

## SEQUENCE LISTING

<110> Duvick, Jonathan P.  
     Gilliam, Jacob T.  
     Maddox, Joyce R.  
     Crasta, Oswald R.  
     Folkerts, Otto

<120> Amino Polyol Amine Oxidase  
     Polynucleotides and Related Polypeptides and Methods of Use

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<150> US 60/092,936  
 <151> 1998-07-15

<150> US 09/352,168  
 <151> 1999-07-12

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 tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcgccg ggaagaggtg 300  
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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt 144  
Glu Ala Met Asp Arg Val Gly Lys Thr Leu Ser Val Gln Ser Gly  
35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192  
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240  
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288  
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336  
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
100 105 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384  
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile  
115 120 125

gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg 432  
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
130 135 140

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145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg	672
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met	
210 215 220	
tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct	720
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225 230 235 240	
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Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly	
245 250 255	
gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg	816
Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu	
260 265 270	
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Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala	
275 280 285	
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Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val	
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Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val	
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gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg	1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg	
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Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp	
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caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
370 375 380	
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga	1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	

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405 410 415				
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr				1296
420 425 430				
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln				1344
435 440 445				
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala				1386
450 455 460				
tag				1389
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Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp				
50 55 60				
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu				
65 70 75 80				
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp				
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Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu				
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Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg				
130 135 140				
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu				
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Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly				
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys				
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Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met				
210 215 220				
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala				
225 230 235 240				
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly				
245 250 255				
Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu				
260 265 270				
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala				
275 280 285				

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
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 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
 305 310 315 320  
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
 325 330 335  
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg  
 340 345 350  
 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
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 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
 370 375 380  
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 385 390 395 400  
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
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 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
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ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
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Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
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Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
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Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat	872
Val Phe Arg Ser Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
275 280 285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg	968
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290 295 300 305	
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Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
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Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys			
340	345	350	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa			1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln			
355	360	365	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc			1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala			
370	375	380	385
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Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
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ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg			1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala			
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Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp			
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Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp			
85	90	95	
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu			
100	105	110	
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile			
115	120	125	
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg			
130	135	140	
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu			
145	150	155	160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
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 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
                  180                 185                 190  
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
                  195                 200                 205  
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
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 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
                  225                 230                 235                 240  
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
                  245                 250                 255  
 Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu  
                  260                 265                 270  
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
                  275                 280                 285  
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
                  290                 295                 300  
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
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 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
                  325                 330                 335  
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg  
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 Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp  
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 Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro  
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 Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly  
                  385                 390                 395                 400  
 Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser  
                  405                 410                 415  
 Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr  
                  420                 425                 430  
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln  
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 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
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 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
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 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
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 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp  
   85                 90                 95  
 Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
   100                 105                 110  
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Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly		
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys		
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Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly		
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Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly		
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Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro		
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Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln		
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His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr		
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Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn		
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Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly		
	355	365
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Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr		
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	405	415
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Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val

48

96

20	25	30	
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ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50 55 60			192
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65 70 75 80			240
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 90 95			288
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100 105 110			336
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125			384
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140			432
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160			480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175			528
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190			576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205			624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 210 215 220			672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240			720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255			768
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270			816

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
cgx aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385 390 395 400	1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405 410 415	1248
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420 425 430	1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435 440 445	1344
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450 455 460	1389
tag	1392
<210> 11	
<211> 463	
<212> PRT	
<213> <i>Exophiala spinifera</i>	
<220>	
<223> Extra lysine in the polypeptide sequence of K:trAPAO, 463 aa.	
<400> 11	
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
     20                 25                 30  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
     35                 40                 45  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
     50                 55                 60  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
     65                 70                 75                 80  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
     85                 90                 95  
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
     100                105                110  
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
     115                120                125  
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
     130                135                140  
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
     145                150                155                160  
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
     165                170                175  
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
     180                185                190  
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
     195                200                205  
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
     210                215                220  
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
     225                230                235                240  
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
     245                250                255  
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
     260                265                270  
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
     275                280                285  
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
     290                295                300  
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
     305                310                315                320  
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
     325                330                335  
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
     340                345                350  
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
     355                360                365  
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
     370                375                380  
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
     385                390                395                400  
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
     405                410                415  
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
     420                425                430  
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
     435                440                445  
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
     450                455                460

&lt;210&gt; 12

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>  
 <223> Primer sequence designed for cloning DNA into  
 expression vectors, N23256

<400> 12  
 ggggaattca aagacaacgt tgccggacgtg gtag

34

<210> 13  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer sequence designed for cloning DNA into  
 expression vectors, N23259

<400> 13  
 ggggcggccg cctatgctgc tggcaccagg ctag

34

<210> 14  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 14  
 tggtttcgtt accgacaacc ttgtatccc

29

<210> 15  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide for 5' race, N21968

<400> 15  
 gagttggtcc cagacagact tttgtcgt

28

<210> 16  
 <211> 1673  
 <212> DNA  
 <213> Exophiala spinifera

<220>  
 <221> sig\_peptide  
 <222> (1)...(267)  
 <223> yeast alpha mating factor secretion signal.

<221> CDS  
 <222> (1)...(1662)

<400> 16  
 atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc  
 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser

-85                    -80                    -75

48

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa  
 Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln

-70                    -65                    -60

96

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe -55 -50 -45	144
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu -40 -35 -30	192
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val -25 -20 -15 -10	240
tct ctc gag aaa aga gag gct gaa gtc gaa ttc aaa gac aac gtt gcg Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala -5 1 5	288
gac gtg gta gtg gtc gct ggc ttg agc ggt ttg gag acg gca cgc Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg 10 15 20	336
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp 25 30 35	384
cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr 40 45 50 55	432
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser 60 65 70	480
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln 75 80 85	528
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr 90 95 100	576
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala 105 110 115	624
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 120 125 130 135	672
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 140 145 150	720
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 155 160 165	768
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 170 175 180	816
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	864

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly			
185	190	195	
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga			912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg			
200	205	210	215
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt			960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu			
220	225	230	
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag			1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln			
235	240	245	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga			1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg			
250	255	260	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg			1104
Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu			
265	270	275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat			1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn			
280	285	290	295
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg			1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro			
300	305	310	
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac			1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			
315	320	325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg			1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			
330	335	340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa			1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			
345	350	355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
360	365	370	375
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
380	385	390	
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala			
395	400	405	
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg			1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr			
410	415	420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg			1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp			
425	430	435	



235	240	245
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg		
250	255	260
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu		
265	270	275
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn		
280	285	290
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro		
300	305	310
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp		
315	320	325
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp		
330	335	340
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln		
345	350	355
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala		
360	365	370
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu		
380	385	390
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala		
395	400	405
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr		
410	415	420
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp		
425	430	435
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala		
440	445	450
Glu Val Val Ala Ser Leu Val Pro Ala Ala		
460	465	

<210> 18  
<211> 2079  
<212> DNA  
<213> Unknown

<220>  
<221> CDS  
<222> (1) ... (2076)

<223> GST:K:trAPAO 2079 nt. Translation starting at nt 1  
- 687, gst fusion + polylinker; 688-2076,  
K:trAPAO; 2077-2079, stop codon. For bacterial  
expression.

<221> misc\_feature  
<222> (1) ... (687)  
<223> gst fusion + polylinker

<221> misc\_feature  
<222> (688) ... (2076)  
<223> K:trAPAO

<221> misc\_feature  
<222> (688) ... (690)  
<223> Extra lysine

<400> 18

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1	5
10	15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	20	25	30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg				144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	35	40	45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa				192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	50	55	60	
tta aca cag tct atg gcc atc ata-cgt tat ata gct gac aag cac aac				240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	65	70	75	
atg ttg ggt ggt ttt cca aaa gag cgt gca gag att tca atg ctt gaa				288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	85	90	95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt				336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	100	105	110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa				384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	115	120	125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat				432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	130	135	140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat				480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	145	150	155	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta				528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	165	170	175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac				576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc				624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	195	200	205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt				672
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	210	215	220	
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc				720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	225	230	235	
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt				768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	245	250	255	
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act				816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	260	265	270	

ctg	agc	gta	caa	tcg	ggt	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	864	
Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly		
275						280					285						
gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	912	
Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe		
290						295				300							
gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	960	
Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser		
305				310				315				320					
atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	1008	
Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp		
325						330				335							
tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	1056	
Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro		
340				345			350										
gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	1104	
Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala		
355				360			365										
agc	cct	cag	gcg	aag	cg	ctc	gac	agt	gtg	agc	ttc	g	c	c	t	1152	
Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys		
370				375			380										
gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	1200	
Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile		
385				390			395			400							
aca	cgc	gct	ctc	ggt	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	1248		
Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe		
405						410				415							
ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	1296	
Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser		
420						425				430							
gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	1344	
Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln		
435						440				445							
tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	1392	
Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His		
450						455				460							
ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	1440	
Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr		
465						470				475			480				
gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	1488	
Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val		
485						490				495							
tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	1536	
Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu		
500						505					510						
ccc	gcc	gag	aag	caa	gca	ttg	g	cg	gaa	aat	tct	atc	ctg	ggc	tac	tat	1584

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr			
515	520	525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc			1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly			
530	535	540	
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga			1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg			
545	550	555	560
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg			1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met			
565	570	575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga			1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg			
580	585	590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg			1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly			
595	600	605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag			1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys			
610	615	620	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat			1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp			
625	630	635	640
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat			1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His			
645	650	655	
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg			2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly			
660	665	670	
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg			2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu			
675	680	685	
gtg cca gca gca tag			2079
Val Pro Ala Ala			
690			
<210> 19			
<211> 692			
<212> PRT			
<213> Unknown			
<220>			
<223> GST:K:trAPAO; GST + linker, aa 1-229; K:trAPAO, aa			
230-692			
<400> 19			
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro			
1	5	10	15
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu			
20	25	30	

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly  
 225 230 235 240  
 Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly  
 245 250 255  
 Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr  
 260 265 270  
 Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly  
 275 280 285  
 Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe  
 290 295 300  
 Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser  
 305 310 315 320  
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp  
 325 330 335  
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro  
 340 345 350  
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala  
 355 360 365  
 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
 370 375 380  
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile  
 385 390 395 400  
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe  
 405 410 415  
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser  
 420 425 430  
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln  
 435 440 445  
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His  
 450 455 460  
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr  
 465 470 475 480  
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val  
 485 490 495  
 Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu  
 500 505 510  
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr  
 515 520 525

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly  
 530 535 540  
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
 545 550 555 560  
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
 565 570 575  
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
 580 585 590  
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
 595 600 605  
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
 610 615 620  
 Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
 625 630 635 640  
 Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
 645 650 655  
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
 660 665 670  
 Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
 675 680 685  
 Val Pro Ala Ala  
 690

<210> 20  
 <211> 1464  
 <212> DNA  
 <213> Unknown

<220>  
 <221> sig\_peptide  
 <222> (1)...(72)  
 <223> Barley Alpha Amylase signal sequence.

<221> misc\_feature  
 <222> (73)...(1464)  
 <223> K:trAPAOcDNA

<221> CDS  
 <222> (1)...(1461)

<223> Nucleotide sequence of K:trAPAO translational  
 fusion with barley alpha amylase signal sequence,  
 for expression and secretion of the mature trAPAO  
 in maize. Nucleotides 1-72, barley alpha amylase  
 signal sequence, nucleotides 73-75, added lysine  
 residue; nucleotides 76 -1464 , trAPAO cDNA.

<221> misc\_feature  
 <222> (73)...(75)  
 <223> Added lysine residue

<400> 20

atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc  
 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
 -20 -15 -10

48

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta  
 Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val  
 -5 1 5

96

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag  
 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln

144

10	15	20														
gcc	gcc	ggt	ctg	tcc	tgc	ctc	gtt	gag	gct	atg	gat	cgt	gta	ggg	192	
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	
25					30					35				40		
gga	aag	act	ctg	agc	gta	caa	tcg	ggt	ccc	ggc	agg	acg	act	atc	aac	240
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	
					45				50				55			
gac	ctc	ggc	gct	gct	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	tcc	288
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	
					60				65				70			
aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	act	336
Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Ile	Gln	Arg	Thr	Thr	
					75				80				85			
gga	aat	tca	atc	cat	caa	gca	caa	gac	ggt	aca	acc	act	aca	gct	cct	384
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	
					90				95				100			
tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gct	gaa	432
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	
					105				110				115		120	
ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	gac	480
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	
					125				130				135			
ctc	aag	gct	agc	cct	cag	gct	gct	aag	cg	ctc	gac	agt	gt	agc	ttc	528
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	
					140				145				150			
cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc	ggc	gta	gca	576
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	
					155				160				165			
aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	gt	gaa	gcc	cac	gag	atc	agc	624
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Ala	His	Glu	Ile	Ser		
					170				175				180			
atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	gcc	acc	ggt	ctc	agt	aat	672
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	
					185				190				195		200	
att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg	cag	tat	atg	cga	tgc	aaa	aca	720
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	
					205				210				215			
ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	tca	aag	gaa	ctt	gtt	cca	ggc	768
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	
					220				225				230			
tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	gaa	att	gag	cag	tcg	gca	tcc	816
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	
					235				240				245			
ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	agc	aaa	aag	864
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	
					250				255				260			

gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser 265 270 275 280	912
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu 285 290 295	960
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg 300 305 310	1008
gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser 315 320 325	1056
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr 330 335 340	1104
tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys 345 350 355 360	1152
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu 365 370 375	1200
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu 380 385 390	1248
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly 395 400 405	1296
ctg aac gat ctc atc aca ctg ggt tcg qcg ctc aga acg ccg ttc aag Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys 410 415 420	1344
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr 425 430 435 440	1392
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val 445 450 455	1440
gct agc ctg gtg cca gca gca tag Ala Ser Leu Val Pro Ala Ala 460	1464

<210> 21  
<211> 487  
<212> PRT  
<213> Unknown

<220>  
<221> SIGNAL  
<222> (1)...(24)

<223> K:trAPAO translational fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize.

<400> 21

Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly
					-20				-15					-10	
Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Lys	Asp	Asn	Val	Ala	Asp	Val	Val
					-5			1					5		
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
					10			15		20					
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
					25			30		35			40		
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
					45			50			55				
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser
					60			65			70				
Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
					75			80			85				
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro
					90			95		100					
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
					105			110		115			120		
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp
					125			130			135				
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala
					140			145			150				
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala
					155			160			165				
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser
					170			175			180				
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn
					185			190			195			200	
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr
					205			210			215				
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly
					220			225			230				
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser
					235			240			245				
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys
					250			255			260				
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser
					265			270			275			280	
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu
					285			290			295				
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg
					300			305			310				
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser
					315			320			325				
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr
					330			335			340				
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys
					345			350			355			360	
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu
					365			370			375				
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu
					380			385			390				
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly
					395			400			405				
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys
					410			415			420				
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr



180	185	190	
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 195	200	205	624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210	215	220	672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 225	230	235	720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245	250	255	768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260	265	270	816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275	280	285	864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290	295	300	912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305	310	315	960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325	330	335	1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340	345	350	1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355	360	365	1104
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370	375	380	1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385	390	395	1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405	410	415	1248
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420	425	430	1296

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435 440 445	1344
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450 455 460	1392
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 465 470 475 480	1440
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 485 490 495	1488
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 500 505 510	1536
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 515 520 525	1584
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 530 535 540	1632
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 545 550 555 560	1680
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 565 570 575	1728
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 580 585 590	1776
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala 595 600	1803
<p>&lt;210&gt; 23  &lt;211&gt; 600  &lt;212&gt; PRT  &lt;213&gt; <i>Exophiala spinifera</i></p> <p>&lt;400&gt; 23</p> <p>Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro  1 5 10 15  Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  20 25 30  Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  35 40 45  Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  50 55 60  Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  65 70 75 80  Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly</p>	

85	90	95
Leu Lys Ala Thr Phe Ala Leu Asp Arg	Leu Pro Pro Cys	Thr Leu Val
100	105	110
Pro Val Ser Ala Leu Ser Ser Pro	Glu Tyr Leu Phe Glu Val	Asp Ala
115	120	125
Thr Ala Leu Val Pro Gly His	Thr Thr Pro Asp Asn Val	Ala Asp Val
130	135	140
Val Val Val Gly Ala Gly	Leu Ser Gly Leu Glu Thr Ala Arg	Lys Val
145	150	155
Gln Ala Ala Gly	Leu Ser Cys Leu Val	Leu Glu Ala Met Asp Arg Val
165	170	175
Gly Gly Lys Thr Leu Ser Val Gln	Ser Gly Pro Gly Arg	Thr Thr Ile
180	185	190
Asn Asp Leu Gly Ala Ala Trp	Ile Asn Asp Ser Asn Gln	Ser Glu Val
195	200	205
Ser Arg Leu Phe Glu Arg	Phe His Leu Glu Gly	Glu Leu Gln Arg Thr
210	215	220
Thr Gly Asn Ser Ile His	Gln Ala Gln Asp	Gly Thr Thr Thr Ala
225	230	235
Pro Tyr Gly Asp Ser	Leu Leu Ser Glu Glu Val	Ala Ser Ala Leu Ala
245	250	255
Glu Leu Leu Pro Val Trp Ser Gln	Leu Ile Glu Glu His	Ser Leu Gln
260	265	270
Asp Leu Lys Ala Ser Pro Gln	Ala Lys Arg Leu Asp	Ser Val Ser Phe
275	280	285
Ala His Tyr Cys Glu Lys	Glu Leu Asn Leu Pro	Ala Val Leu Gly Val
290	295	300
Ala Asn Gln Ile Thr Arg	Ala Leu Leu Gly Val	Glu Ala His Glu Ile
305	310	315
Ser Met Leu Phe Leu Thr Asp Tyr	Ile Lys Ser Ala Thr Gly	Leu Ser
325	330	335
Asn Ile Phe Ser Asp Lys	Lys Asp Gly Gly	Gln Tyr Met Arg Cys Lys
340	345	350
Thr Gly Met Gln Ser Ile Cys	His Ala Met Ser Lys	Glu Leu Val Pro
355	360	365
Gly Ser Val His Leu Asn Thr	Pro Val Ala Glu	Ile Glu Gln Ser Ala
370	375	380
Ser Gly Cys Thr Val Arg	Ser Ala Ser Gly	Ala Val Phe Arg Ser Lys
385	390	395
Lys Val Val Val Ser	Leu Pro Thr Thr	Leu Tyr Pro Thr Leu Thr Phe
405	410	415
Ser Pro Pro Leu Pro Ala Glu	Lys Gln Ala	Leu Ala Glu Asn Ser Ile
420	425	430
Leu Gly Tyr Tyr Ser Lys Ile Val	Phe Val Trp Asp	Lys Pro Trp Trp
435	440	445
Arg Glu Gln Gly Phe Ser	Gly Val Leu Gln Ser	Ser Cys Asp Pro Ile
450	455	460
Ser Phe Ala Arg Asp	Thr Ser Ile Asp Val	Asp Arg Gln Trp Ser Ile
465	470	475
Thr Cys Phe Met Val	Gly Asp Pro Gly Arg	Lys Trp Ser Gln Gln Ser
485	490	495
Lys Gln Val Arg Gln	Lys Ser Val Trp Asp	Gln Leu Arg Ala Ala Tyr
500	505	510
Glu Asn Ala Gly Ala Gln	Val Pro Glu Pro Ala Asn	Val Leu Glu Ile
515	520	525
Glu Trp Ser Lys Gln	Gln Tyr Phe Gln Gly	Ala Pro Ser Ala Val Tyr
530	535	540
Gly Leu Asn Asp Leu Ile	Thr Leu Gly Ser	Ala Leu Arg Thr Pro Phe
545	550	555
Lys Ser Val His Phe Val	Gly Thr Glu Thr	Ser Leu Val Trp Lys Gly
565	570	575
Tyr Met Glu Gly Ala Ile	Arg Ser Gly Gln	Arg Gly Ala Ala Glu Val



cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly 75 80 85	336
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu 90 95 100	384
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tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala 125 130 135	480
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu 140 145 150	528
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly 155 160 165	576
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala 170 175 180	624
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala 185 190 195 200	672
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro 205 210 215	720
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe 220 225 230	768
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu 235 240 245	816
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp 250 255 260	864
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu 265 270 275 280	912
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg 285 290 295	960
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala 300 305 310	1008
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr	1056

315	320	325	
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt			1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu			
330	335	340	
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag			1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln			
345	350	355	360
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc			1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
365	370	375	
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac			1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr			
380	385	390	
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg			1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val			
395	400	405	
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca			1344
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala			
410	415	420	
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc			1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala			
425	430	435	440
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa			1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln			
445	450	455	
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt			1488
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val			
460	465	470	
gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt			1536
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
475	480	485	
tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc			1584
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly			
490	495	500	
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg			1632
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val			
505	510	515	520
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc			1680
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
525	530	535	
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag ggc atg gat cgt gta			1728
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val			
540	545	550	
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc			1776
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile			
555	560	565	

aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570 575 580	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585 590 595 600	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 745 750 755 760	2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 765 770 775	2400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 780 785 790	2448
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 795 800 805	2496
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	2544

810	815	820	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 825 830 835 840			2592
tca ttt gcc aga gat acc acc gac gtc gat cga caa tgg tcc att Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile 845 850 855			2640
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser 860 865 870			2688
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr 875 880 885			2736
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile 890 895 900			2784
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr 905 910 915 920			2832
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe 925 930 935			2880
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly 940 945 950			2928
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val 955 960 965			2976
gtg gct agc ctg gtg cca gca gca tag Val Ala Ser Leu Val Pro Ala Ala 970 975			3003
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<pre> &lt;220&gt; &lt;221&gt; SIGNAL &lt;222&gt; (1)...(24) </pre>			
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45	50	55	
Ala Tyr Gly Pro Ala Cys Pro Gln Gln	Phe Asn Tyr Pro Glu Glu	Leu	
60	65	70	
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro	Pro Pro Ser Ala Gly		
75	80	85	
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile	Tyr Val Pro Gly Thr Glu		
90	95	100	
Asn Thr Asn Lys Ala Val Met Val Trp Ile	Tyr Gly Gly Ala Leu	Glu	
105	110	115	120
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly	Ala Ser Phe Ala Ala		
125	130	135	
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg	Thr Asn Ile Leu		
140	145	150	
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln	Arg Asn Leu Gly		
155	160	165	
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val	Gln Arg Asn Ile Ala		
170	175	180	
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile	Phe Gly Gln Ser Ala		
185	190	195	200
Gly Gly Arg Ser Val Asp Val Leu Leu Thr	Ser Met Pro His Asn Pro		
205	210	215	
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val	Ala Asn Tyr Asn Phe		
220	225	230	
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr	Thr Val Gln Ala Leu		
235	240	245	
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys	Met Arg Arg Val Asp		
250	255	260	
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu	Gly Leu Gly Phe Glu		
265	270	275	280
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr	Arg Ser Glu Thr Ala Arg		
285	290	295	
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu	Val Gly Thr Val Ala		
300	305	310	
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu	Asn Asp Thr Gln Ala Tyr		
315	320	325	
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu	Tyr Gln Thr Leu Leu		
330	335	340	
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile	Gly Ser Pro Gln Asp Gln		
345	350	355	360
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe	Gln Cys Pro Ser Ala Ile		
365	370	375	
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile	Pro Ser Trp Arg Tyr Tyr		
380	385	390	
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu	Phe Pro Gly Ser Glu Val		
395	400	405	
Tyr His Ser Ser Glu Val Gly Met Val Phe	Gly Thr Tyr Pro Val Ala		
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Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser	Lys Tyr Met Gln Gly Ala		
425	430	435	440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn	Gly Pro Gly Trp Lys Gln		
445	450	455	
Val Pro Asn Val Ala Ala Leu Gly Ser Pro	Gly Lys Ala Ile Gln Val		
460	465	470	
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg	Cys Ala Leu Tyr Thr Arg		
475	480	485	
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro	Arg Thr Phe Gly Gly		
490	495	500	
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val	Ala Asp Val		
505	510	515	520
Val Val Val Gly Ala Gly Leu Ser Gly Leu	Glu Thr Ala Arg Lys Val		
525	530	535	
Gln Ala Ala Gly Leu Ser Cys Leu Val	Leu Glu Ala Met Asp Arg Val		

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Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile			
555	560	565	
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val			
570	575	580	
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr			
585	590	595	600
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala			
605	610	615	
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
620	625	630	
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln			
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Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
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Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
665	670	675	680
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
685	690	695	
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
700	705	710	
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
715	720	725	
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
730	735	740	
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
745	750	755	760
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
765	770	775	
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
780	785	790	
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
795	800	805	
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
810	815	820	
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
825	830	835	840
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
845	850	855	
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
860	865	870	
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			
875	880	885	
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile			
890	895	900	
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
905	910	915	920
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
925	930	935	
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
940	945	950	
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
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      mature: artificial spacer: and K:trAPAO. For
      plant expression.

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<221> misc_feature
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      -20           -15           -10

ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc 96
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
      -5           1           5

gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc 144
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
      10          15          20

gga ata ccc tat gca gcg ccg gtg ggc ggg ctg cgt tgg aag ccg 192
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
      25          30          35          40

ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt 240
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
      45          50          55

ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc 288
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
      60          65          70

ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca 336
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
      75          80          85

ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc 384
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
      90          95          100

ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg 432
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala

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ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly 380	385	390	1248	
aga gcg ccc gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val 395	400	405	1296	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro 410	415	420	1344	
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val 425	430	435	440	1392
cggttcgcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro 445	450	455	1440	
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg 460	465	470	1488	
gctgctgtgtgtccggatccatccccttgcgatggc Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly 475	480	485	1536	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc Ala Lys Ala Gly Gly Ser Gly Gly Ser Gly Gly Ser 490	495	500	1584	
aaa gac aac gtt gct gac gtt gta gtt gtt ggc gct ggc ttg agc ggt Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly 505	510	515	520	1632
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val 525	530	535	1680	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 540	545	550	1728	
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 555	560	565	1776	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 570	575	580	1824	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 585	590	595	600	1872
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu				1920

605	610	615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 620	625	630	1968
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 635	640	645	2016
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 650	655	660	2064
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 665	670	675	2112
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 685	690	695	2160
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 700	705	710	2208
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala 715	720	725	2256
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 730	735	740	2304
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 745	750	755	2352
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 765	770	775	2400
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 780	785	790	2448
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 795	800	805	2496
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 810	815	820	2544
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 825	830	835	2592
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 845	850	855	2640

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg 2688  
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
 860 865 870

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag 2736  
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 875 880 885

ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa 2784  
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 890 895 900

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 2832  
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
 905 910 915 920

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 2880  
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
 925 930 935

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 2928  
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 940 945 950

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca 2973  
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
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tag 2976

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 Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr  
 -5 1 5  
 Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg  
 10 15 20  
 Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro  
 25 30 35 40  
 Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe  
 45 50 55  
 Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala  
 60 65 70  
 Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser  
 75 80 85  
 Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly  
 90 95 100  
 Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala  
 105 110 115 120  
 Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn  
 125 130 135  
 Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr  
 140 145 150

Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg  
 155 160 165  
 Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val  
 170 175 180  
 Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu  
 185 190 195 200  
 Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser  
 205 210 215  
 Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser  
 220 225 230  
 Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro  
 235 240 245  
 Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp  
 250 255 260  
 Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu  
 265 270 275 280  
 Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val  
 285 290 295  
 Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly  
 300 305 310  
 Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala  
 315 320 325  
 Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp  
 330 335 340  
 Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn  
 345 350 355 360  
 Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln  
 365 370 375  
 Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly  
 380 385 390  
 Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val  
 395 400 405  
 Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro  
 410 415 420  
 Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val  
 425 430 435 440  
 Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro  
 445 450 455  
 Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg  
 460 465 470  
 Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly  
 475 480 485  
 Ala Lys Ala Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser  
 490 495 500  
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 505 510 515 520  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 525 530 535  
 Leu Glu Ala Met Asp Arg Val Gly Lys Thr Leu Ser Val Gln Ser  
 540 545 550  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 555 560 565  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 570 575 580  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 585 590 595 600  
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
 605 610 615  
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 620 625 630  
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
 635 640 645

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
 650 655 660  
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
 665 670 675 680  
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
 685 690 695  
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
 700 705 710  
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala  
 715 720 725  
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
 730 735 740  
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
 745 750 755 760  
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
 765 770 775  
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
 780 785 790  
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
 795 800 805  
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
 810 815 820  
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
 825 830 835 840  
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
 845 850 855  
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
 860 865 870  
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 875 880 885  
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 890 895 900  
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
 905 910 915 920  
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
 925 930 935  
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
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 955 960 965

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<211> 3618

<212> DNA

<213> Unknown

<220>

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 2227-3615, K:trAPAO, extra lysine; 3616-3618, stop  
 codon. For bacterial expression.

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<222> (1)...(3615)

<221> misc\_feature

<222> (1)...(687)

<223> gast + polylinker

<221> mat\_peptide

<222> (688)...(2190)

<223> espl mat

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1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt ttt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta ttt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205	624
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220	672
gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val 225 230 235 240	720
gtc ggc acg act act gtc ccc ggc acc act gcg acc gtc agc gag Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu 245 250 255	768
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act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly 275 280 285	864
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc cgt gag att Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile 290 295 300	912
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly Glu Ser Glu 305 310 315 320	960
gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn 325 330 335	1008
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp 340 345 350	1056
aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc aat cag gat Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp 355 360 365	1104
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro 370 375 380	1152
gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp 385 390 395 400	1200
caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca gcc ttt ggc Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly 405 410 415	1248
ggg gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg 420 425 430	1296
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg	1344

435	440	445	
gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc ccc aag gga Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly 450 455 460			1392
gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr 465 470 475 480			1440
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485 490 495			1488
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu 500 505 510			1536
gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc acg act ggt Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly 515 520 525			1584
gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly 530 535 540			1632
ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat ctc gag gag Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu 545 550 555 560			1680
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr 565 570 575			1728
ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580 585 590			1776
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595 600 605			1824
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610 615 620			1872
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625 630 635 640			1920
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645 650 655			1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660 665 670			2016
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn 675 680 685			2064

gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser 690 695 700	2112
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr 705 710 715 720	2160
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ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val 740 745 750	2256
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala 755 760 765	2304
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys 770 775 780	2352
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu 785 790 795 800	2400
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu 805 810 815	2448
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn 820 825 830	2496
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly 835 840 845	2544
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 850 855 860	2592
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 865 870 875 880	2640
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr 885 890 895	2688
tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln 900 905 910	2736
atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu 915 920 925	2784
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe	2832

930	935	940	
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met	945 950	955	2880 960
cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val	965	970	2928 975
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys	980	985	2976 990
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val	995	1000	3024 1005
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro	1010	1015	3072 1020
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr	1025	1030	3120 1035
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln	1045	1050	3168 1055
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala	1060	1065	3216 1070
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe	1075	1080	3264 1085
atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val	1090	1095	3312 1100
cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala	1105	1110	3360 1115
ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser	1125	1130	3408 1135
aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn	1140	1145	3456 1150
gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val	1155	1160	3504 1165
cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu	1170	1175	3552 1180

ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc 3600  
 Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser  
 1185 1190 1195 1200

ctg gtg cca gca gca tag 3618  
 Leu Val Pro Ala Ala  
 1205

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 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205  
 Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220  
 Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val 225 230 235 240  
 Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu 245 250 255  
 Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro 260 265 270  
 Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly 275 280 285  
 Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile 290 295 300  
 Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu 305 310 315 320  
 Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn 325 330 335  
 Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp 340 345 350  
 Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp 355 360 365  
 Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro

370	375	380
Ala	Ala	Pro
Gln	Leu	Pro
385	390	395
Gln	Arg	Phe
Arg	Phe	Ala
Leu	Asp	Trp
405	410	415
Gly	Asp	Pro
Asp	Arg	Lys
420	425	430
Ser	Val	Asp
Asp	Val	Leu
Leu	Leu	Thr
435	440	445
Ala	Ala	Ile
Ala	Met	Glu
450	455	460
Gly	Val	Ala
Asn	Tyr	Asn
Phe	Pro	Phe
465	470	475
Gly	Asp	Pro
Asp	Val	Leu
Leu	Leu	Thr
Ser	Met	Pro
480	485	495
His	Asn	Pro
Asn	Pro	Pro
Phe	Arg	Arg
Arg	Arg	Arg
495	500	510
Val	Asn	Thr
Asn	Thr	Ile
505	510	515
Glu	Gly	Leu
Gly	Leu	Gly
515	520	525
Phe	Asp	Leu
Asp	Leu	Ala
525	530	535
Asp	Ile	Ala
Ala	Arg	Val
535	540	545
Pro	Val	Leu
545	550	555
Val	Gly	Glu
Gly	Glu	Asn
Asn	Asp	Thr
555	560	565
Gln	Ala	Thr
565	570	575
Pro	Ile	Gly
Ile	Ser	Pro
Gly	Ile	Gly
580	585	590
Ser	Pro	Gln
Gly	Gly	Asp
595	600	605
Asp	Ile	Asn
Ser	Arg	Arg
Asn	Gly	Ile
Arg	Pro	Pro
Gly	Leu	Ser
610	615	620
Trp	Arg	Tyr
Arg	Tyr	Tyr
Tyr	Tyr	Asn
Asn	Ala	Ala
620	625	630
Thr	Phe	Glu
Glu	Asn	Leu
Asn	Glu	Leu
635	640	645
Phe	Pro	Gly
645	650	655
Gly	Gly	Asn
655	660	665
Asn	Pro	Met
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Asn	Gly	Asn
675	680	685
Pro	Ala	Lys
685	690	695
Asn	Pro	Gly
695	700	705
Gly	Leu	Ser
705	710	715
Asp	Ile	Asp
Gln	Arg	Cys
715	720	725
Ala	Leu	Ala
725	730	735
Thr	Ile	Ala
735	740	745
Arg	Pro	Arg
745	750	755
Gly	Gly	Gly
755	760	765
Gly	Leu	Ser
765	770	775
Cys	Leu	Val
775	780	785
Leu	Glu	Ala
785	790	795
Ala	Met	Asp
795	800	805
Asp	Arg	Arg
805	810	815
Phe	Glu	Phe
815	820	825
Arg	His	Leu
825	830	835
Gly	Glu	Gly
835	840	845
Asp	Leu	Leu
845	850	855
Leu	Leu	Ser
855	860	865
Ser	Leu	Glu
Gly	Glu	His
865	870	875
Asp	Leu	Lys

865	870	875	880
Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr			
885	890	895	
Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln			
900	905	910	
Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu			
915	920	925	
Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe			
930	935	940	
Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met			
945	950	955	960
Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val			
965	970	975	
His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys			
980	985	990	
Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val			
995	1000	1005	
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro			
1010	1015	1020	
Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr			
1025	1030	1035	1040
Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln			
1045	1050	1055	
Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala			
1060	1065	1070	
Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe			
1075	1080	1085	
Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val			
1090	1095	1100	
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala			
1105	1110	1115	1120
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser			
1125	1130	1135	
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn			
1140	1145	1150	
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val			
1155	1160	1165	
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu			
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Leu Val Pro Ala Ala			
1205			

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<211> 3591

<212> DNA

<213> Unknown

<220>

<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression vector pGEX-4T-1 or similar vector.

gst:BEST1:sp:K:trAPAO fusion, 3591 nt. 1-687 gst + polylinker, 688-2163, BEST1 mature; 2164-2199, spacer, 2200-3588, K:trAPAO

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<223> gst + polylinker

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1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	

gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac		576	
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc		624	
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
195	200	205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt		672	
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
210	215	220	
gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc		720	
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly			
225	230	235	240
cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc gga ata ccc		768	
Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro			
245	250	255	
tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac		816	
Tyr Ala Ala Pro Pro Val Gly Leu Arg Trp Lys Pro Pro Gln His			
260	265	270	
gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac		864	
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp			
275	280	285	
tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg		912	
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val			
290	295	300	
agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa		960	
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys			
305	310	315	320
ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc		1008	
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Phe Ala			
325	330	335	
ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga		1056	
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg			
340	345	350	
cag ggc gtc gtc gtg acg ttt aac tat cgg acg aac atc ctg ggc		1104	
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly			
355	360	365	
ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg		1152	
Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser			
370	375	380	
ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag		1200	
Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln			
385	390	395	400
agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt		1248	
Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe			
405	410	415	
ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg		1296	

Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro			
420	425	430	
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg			1344
Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu			
435	440	445	
acg cga ccg ctc gcg acg ctc gcc gac agc gcc tcg ggc gag cgc			1392
Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg			
450	455	460	
ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg			1440
Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu			
465	470	475	480
atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac ctg cgc agg			1488
Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg			
485	490	495	
ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc			1536
Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr			
500	505	510	
gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg			1584
Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu			
515	520	525	
atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg cgc gcg ccg			1632
Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro			
530	535	540	
atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt ggc			1680
Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly			
545	550	555	560
gac caa gcc gcc gtg gcg tgc tat ccc ctc gac ggc cgg gcc			1728
Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala			
565	570	575	
acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat cag ttc aat			1776
Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn			
580	585	590	
cgg ggg gtc tcg gcc ttc tcg gaa ggc ctt gtg cgc cag ggc gcg ccc			1824
Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro			
595	600	605	
gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga aga ggc cgc			1872
Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Arg Ala Pro			
610	615	620	
gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc			1920
Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu			
625	630	635	640
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc			1968
Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala			
645	650	655	
gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc			2016
Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala			
660	665	670	

aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct	2064
Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser	
675 680 685	
acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc gcg gtc	2112
Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val	
690 695 700	
gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc gcc aag gcg	2160
Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala	
705 710 715 720	
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac	2208
Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn	
725 730 735	
gtt gcg gac gtg gta gtg gtc gct ggc ttg agc ggt ttg gag acg	2256
Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr	
740 745 750	
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg	2304
Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala	
755 760 765	
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc	2352
Met Asp Arg Val Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly	
770 775 780	
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac	2400
Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn	
785 790 795 800	
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag	2448
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu	
805 810 815	
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca	2496
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr	
820 825 830	
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca	2544
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala	
835 840 845	
agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag	2592
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu	
850 855 860	
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac	2640
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp	
865 870 875 880	
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct	2688
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala	
885 890 895	
gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa	2736
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu	
900 905 910	
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc	2784

Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala			
915	920	925	
acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat			2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr			
930	935	940	
atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag			2880
Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys			
945	950	955	960
gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att			2928
Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile			
965	970	975	
gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtc			2976
Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val			
980	985	990	
ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc			3024
Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro			
995	1000	1005	
acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg			3072
Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala			
1010	1015	1020	
gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac			3120
Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp			
1025	1030	1035	1040
aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc			3168
Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser			
1045	1050	1055	
tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga			3216
Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg			
1060	1065	1070	
caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg			3264
Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp			
1075	1080	1085	
tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc			3312
Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu			
1090	1095	1100	
ccg gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac			3360
Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn			
1105	1110	1115	1120
gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg			3408
Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro			
1125	1130	1135	
agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc			3456
Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu			
1140	1145	1150	
aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta			3504
Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu			
1155	1160	1165	

gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt 3552  
 Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly  
 1170 1175 1180

gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 3591  
Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
1185 . 1190 1195

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<211> 1196  
<212> PRT  
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<400> 31

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				20				25					30		
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
				35				40				45			
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys

50	55	60	
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
65	70	75	80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
85	90	95	
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
100	105	110	
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
115	120	125	
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
130	135	140	
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
145	150	155	160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
165	170	175	
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
180	185	190	
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
195	200	205	
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
210	215	220	
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly			
225	230	235	240
Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro			
245	250	255	
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His			
260	265	270	
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp			
275	280	285	
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val			
290	295	300	
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys			
305	310	315	320
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Phe Ala			
325	330	335	
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg			
340	345	350	
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly			

355	360	365													
Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr	Gly	Thr	Ser
370						375					380				
Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg	Trp	Val	Gln
385						390					395				400
Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val	Thr	Val	Phe
											405				415
Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu	Thr	Ser	Pro
											420				430
Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	Pro	Gly	Leu
											435				445
Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	Gly	Glu	Arg
											450				460
Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	Ala	Thr	Leu
											465				480
Met	Ala	Arg	Ala	Asp	Ala	Ala	Arg	Pro	Ala	Ser	Arg	Asp	Leu	Arg	Arg
											485				495
Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	Pro	Gln	Thr
											500				510
Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	Arg	Val	Leu
											515				525
Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	Arg	Ala	Pro
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Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	Gln	Phe	Gly
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Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp	Gly	Arg	Ala
											565				575
Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn	Gln	Phe	Asn
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Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	Gly	Ala	Pro
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Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly	Arg	Ala	Pro
											610				620
Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	Phe	Lys	Leu
											625				640
Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	Thr	Pro	Ala
											645				655
Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	Arg	Phe	Ala
											660				670
Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	Ala	Tyr	Ser
											675				685
Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	Ala	Ala	Val
											690				700
Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	Ala	Lys	Ala
											705				720
Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn		
											725				735
Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr
											740				750
Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala
											755				765
Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly
											770				780
Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn
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Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu
											805				815
Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr
											820				830
Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala
											835				845
Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu

850	855	860
His Ser Leu Gln Asp	Leu Lys Ala Ser Pro	Gln Ala Lys Arg
865	870	875
Ser Val Ser Phe Ala His Tyr Cys	Glu Lys Glu Leu Asn	Leu Pro Ala
885	890	895
Val Leu Gly Val Ala Asn Gln	Ile Thr Arg Ala Leu	Leu Gly Val Glu
900	905	910
Ala His Glu Ile Ser Met Leu Phe	Leu Thr Asp Tyr Ile	Lys Ser Ala
915	920	925
Thr Gly Leu Ser Asn Ile Phe	Ser Asp Lys Lys Asp	Gly Gly Gln Tyr
930	935	940
Met Arg Cys Lys Thr Gly	Met Gln Ser Ile Cys	His Ala Met Ser Lys
945	950	955
Glu Leu Val Pro Gly Ser Val His	Leu Asn Thr Pro Val	Ala Glu Ile
965	970	975
Glu Gln Ser Ala Ser Gly Cys	Thr Val Arg Ser Ala	Ser Gly Ala Val
980	985	990
Phe Arg Ser Lys Lys Val Val	Ser Leu Pro Thr	Thr Leu Tyr Pro
995	1000	1005
Thr Leu Thr Phe Ser Pro Pro	Leu Pro Ala Glu	Lys Gln Ala Leu Ala
1010	1015	1020
Glu Asn Ser Ile Leu Gly Tyr	Tyr Ser Lys Ile Val Phe	Val Trp Asp
1025	1030	1035
Lys Pro Trp Trp Arg Glu Gln Gly	Phe Ser Gly Val	Leu Gln Ser Ser
1045	1050	1055
Cys Asp Pro Ile Ser Phe Ala Arg	Asp Thr Ser Ile Asp	Val Asp Arg
1060	1065	1070
Gln Trp Ser Ile Thr Cys Phe	Met Val Gly Asp Pro	Gly Arg Lys Trp
1075	1080	1085
Ser Gln Gln Ser Lys Gln Val Arg	Gln Lys Ser Val	Trp Asp Gln Leu
1090	1095	1100
Arg Ala Ala Tyr Glu Asn Ala Gly	Ala Gln Val Pro	Glu Pro Ala Asn
1105	1110	1115
Val Leu Glu Ile Glu Trp Ser Lys	Gln Gln Tyr Phe	Gln Gly Ala Pro
1125	1130	1135
Ser Ala Val Tyr Glu Leu Asn Asp	Leu Ile Thr Leu Gly	Ser Ala Leu
1140	1145	1150
Arg Thr Pro Phe Lys Ser Val His	Phe Val Gly	Thr Glu Thr Ser Leu
1155	1160	1165
Val Trp Lys Gly Tyr Met Glu	Gly Ala Ile Arg	Ser Gly Gln Arg Gly
1170	1175	1180
Ala Ala Glu Val Val Ala Ser	Leu Val Pro	Ala Ala
1185	1190	1195

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<211> 2490

<212> DNA

<213> Unknown

<220>

<223> GST:glyc(-)APAO open reading frame, 2490 nt; GST and linker, nt 1-687; Glyc (-) APAO, nt 688-2490; mutation in putative glycosylation sites in bold and underlined, nt 1288-1290 (AAT->TCC) and nt 1303-1305 (AGC->AAC).

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<221> misc\_feature

<222> (1)...(687)

<223> GST and linker

<221> misc\_feature  
 <222> (688)...(2490)  
 <223> Glyc (-) APAO

<221> mutation  
 <222> (1288)...(1290)  
 <223> mutation in putative glycosylation site (AAT->TCC)

<221> mutation  
 <222> (1303)...(1305)  
 <223> mutation in putative glycosylation site (AGC->AAC)

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205	624
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220	672
gga tcc ccg gaa ttc atg gca ctt gca ccg agc tac atc aat ccc cca Gly Ser Pro Glu Phe Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro 225 230 235 240	720
aac gtc gcc tcc cca gca ggg tat tct cac gtc ggc gta ggc cca gac Asn Val Ala Ser Pro Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp 245 250 255	768
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ggc gtg aca gac cct gcc tac gag aaa cag gtt gcc caa gca ttc gcc Gly Val Thr Asp Pro Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala 275 280 285	864
aat ctg cga gct tgc ctt gct gca gtt gga gcc act tca aac gac gtc Asn Leu Arg Ala Cys Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val 290 295 300	912
acc aag ctc aat tac tac atc gtc gac tac gcc ccg agc aaa ctc acc Thr Lys Leu Asn Tyr Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr 305 310 315 320	960
gca att gga gat ggg ctg aag gct acc ttt gcc ctt gac agg ctc cct Ala Ile Gly Asp Gly Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro 325 330 335	1008
cct tgc acg ctg gtg cca gtg tcg gcc ttg tct tca cct gaa tac ctc Pro Cys Thr Leu Val Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu 340 345 350	1056
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gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro 405 410 415	1248
ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc tcc gac agc Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Ser Asp Ser 420 425 430	1296
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450	455	460	
aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val			1440
465	470	475	480
gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu			1488
485	490	495	
gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu			1536
500	505	510	
gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro			1584
515	520	525	
gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val			1632
530	535	540	
gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser			1680
545	550	555	560
gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln			1728
565	570	575	
tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser			1776
580	585	590	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu			1824
595	600	605	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala			1872
610	615	620	
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625	630	635	640
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu			1968
645	650	655	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp			2016
660	665	670	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser			2064
675	680	685	

agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat	2112		
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp			
690	695		
695	700		
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cg aag	2160		
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys			
705	710		
715	720		
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa	2208		
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln			
725	730		
735			
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc	2256		
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala			
740	745		
750			
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct	2304		
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala			
755	760		
765			
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg	2352		
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala			
770	775		
780			
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct	2400		
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			
785	790		
795	800		
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Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg			
805	810		
815			
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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
35	40	45	
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
50	55	60	
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
65	70	75	80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
85	90	95	
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
100	105	110	
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
115	120	125	
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
130	135	140	
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			

145	150	155	160
Val	Val	Leu	Tyr
Met	Asp	Pro	Met
Cys		Leu	Asp
165		Ala	Phe
Val	Cys	Phe	Gly
Lys	Lys	Lys	Arg
180		Ile	Glu
Leu	Lys	Ser	Ser
185		Ile	Ala
190		Trp	Pro
195		Leu	Gln
200		Gly	Trp
205		Gln	Gly
Thr	Phe	Gly	Gly
210	Asp	His	Asp
Gly	Ser	Pro	Pro
225	Glu	Phe	Met
Asn	Val	Ala	Leu
230	Ser	Pro	Ala
245	Gly	Gly	Tyr
Gly	Gly	Arg	Val
260	Asp	Tyr	Thr
Gly	265	Ile	Ile
270	Val	Ala	Gly
275	Thr	Tyr	Gly
280	Asp	Glu	Gly
Asn	Leu	Pro	Gly
290	Arg	Ala	Tyr
295	Cys	Gly	Val
300	Leu	Leu	Gly
305	Ala	Ala	Ala
310	Val	Val	Gly
315	Gly	Gly	Asp
320	Asp	Asp	Ala
325	Ala	Ala	Ser
330	Gly	Gly	Pro
335	Ile	Ile	Asn
340	Gly	Gly	Asp
345	Leu	Leu	Val
350	Asp	Asp	Thr
355	Ala	Ala	Asp
360	Thr	Thr	Tyr
365	Ala	Ala	Asp
Asn	Val	Asp	Arg
370	Ala	Val	Val
375	Val	Val	Gly
380	Gly	Gly	Ala
385	Ala	Ala	Gly
390	Gly	Leu	Leu
395	Leu	Ser	Cys
400	Glu	Val	Leu
405	Asp	Asp	Val
410	Arg	Gly	Gly
415	Val	Asp	Lys
Gly	Arg	Thr	Thr
420	Thr	Ile	Asn
425	Asp	Asp	Asp
430	Leu	Gly	Leu
Asn	Gln	Val	Val
435	Asn	Ser	Arg
440	Glu	Leu	Phe
445	Val	Gly	Glu
Glu	Leu	Gly	Arg
450	Arg	Thr	Thr
455	Thr	Gly	Asn
460	Asn	Ser	Ser
Thr	Thr	Ile	His
465	Thr	Asp	Gly
470	Thr	Asp	Asp
475	Ala	Ala	Trp
480	Pro	Pro	Ile
Ala	Ser	Val	Val
485	Ala	Leu	Leu
490	Leu	Leu	Pro
495	Leu	Pro	Val
Glu	His	Ser	Val
500	Ser	Leu	Trp
505	Gln	Gly	Ser
510	Asp	Leu	Gly
Asp	Ser	Asp	Gly
515	Ser	Val	Asp
520	Phe	Asp	Asp
525	Ala	His	Gly
Ala	Val	Leu	Gly
530	Gly	Val	Val
535	Ala	Asn	Asn
540	Gln	Ile	Ile
Glu	Glu	Ser	Met
545	Ile	Met	Leu
550	Ser	Leu	Phe
555	Thr	Leu	Leu
560	Asp	Asp	Ser
Ala	Thr	Gly	Tyr
565	Leu	Leu	Cys
570	Ser	Asn	Ile
575	Asp	Ile	Phe
Tyr	Met	Arg	Gly
580	Cys	Cys	Thr
585	Lys	Lys	Arg
590	Thr	Met	Asp
Lys	Glu	Leu	Leu
595	Val	Val	Pro
600	Pro	Gly	Gly
605	Gly	Ser	Ser
Ile	Glu	Gln	Ala
610	Gln	Ser	Ser
615	Ala	Ala	Gly
620	Ser	Gly	Asp
Val	Phe	Arg	Arg
625	Asp	Ser	Ser
630	Lys	Lys	Val
635	Val	Val	Val
640	Val	Val	Ser
Pro	Thr	Leu	Thr
Pro	Phe	Thr	Phe
Pro	Pro	Leu	Pro
Leu	Pro	Ala	Glu
Glu	Lys	Gln	Ala
Leu			Leu

645	650	655
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp		
660	665	670
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser		
675	680	685
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp		
690	695	700
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys		
705	710	715
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln		
725	730	735
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala		
740	745	750
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala		
755	760	765
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala		
770	775	780
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser		
785	790	795
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg		
805	810	815
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
820	825	